CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/284,327   **ENTERED**

CRF Processing Date: 10/4/2001
Edited by:
Verified by: _____ (STIC staff)

- [ ] Changed a file from non-ASCII to ASCII

- [ ] Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- [ ] Edited a format error in the Current Application Data section, specifically:
  _____

- [ ] Edited the Current Application Data section with the actual current number. The number inputted by the applicant was [ ] the prior application data; or [ ] other _____.

- [ ] Added the mandatory heading and subheadings for "Current Application Data".

- [ ] Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- [ ] Changed the spelling of a mandatory field (the headings or subheadings), specifically:
  _____

- [ ] Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
  _____

- [ ] Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
  _____

- [ ] Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- [ ] Inserted colons after headings/subheadings. Headings edited included:
  _____

- [ ] Deleted extra, invalid, headings used by an applicant, specifically:
  _____

- [ ] Deleted: [ ] non-ASCII "garbage" at the beginning/end of files; [ ] secretary initials/filename at end of file; [ ] page numbers throughout text; [ ] other invalid text, such as _____

- [ ] Inserted mandatory headings, specifically: _____

- [ ] Corrected an obvious error in the response, specifically:
  _____

- [ ] Edited identifiers where upper case is used but lower case is required, or vice versa.

- [ ] Corrected an error in the Number of Sequences field, specifically:
  _____

- [ ] A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- [ ] Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

- [✓] Other: Corrected ∠1607 and ∠1707 numeric identifiers
  _____
  _____
  _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.
3/1/95

RAW SEQUENCE LISTING   DATE: 10/04/2001
PATENT APPLICATION: US/09/284,327   TIME: 12:43:06

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\10042001\I284327.raw

```
        3 <110> APPLICANT: Genencor International, Inc.
        6 <120> TITLE OF INVENTION: Novel EGIII-Like Enzymes, DNA Encoding
        7        Such Enzymes and Methods for Producing Such Enzymes
       10 <130> FILE REFERENCE: GC516-2-PCT
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/284,327
C--> 13 <141> CURRENT FILING DATE: 1999-04-10
       15 <160> NUMBER OF SEQ ID NOS: 41
       17 <170> SOFTWARE: FastSEQ for Windows Version 3.0
       19 <210> SEQ ID NO: 1
       20 <211> LENGTH: 5
       21 <212> TYPE: PRT
       22 <213> ORGANISM: Artificial Sequence
       24 <220> FEATURE:
       25 <223> OTHER INFORMATION: Synthetic
       27 <400> SEQUENCE: 1
       28   Asn Asn Leu Trp Gly
       29   1                 5
       31 <210> SEQ ID NO: 2
       32 <211> LENGTH: 5
       33 <212> TYPE: PRT
       34 <213> ORGANISM: Artificial Sequence
       36 <220> FEATURE:
       37 <223> OTHER INFORMATION: Synthetic
       39 <400> SEQUENCE: 2
       40   Glu Leu Met Ile Trp
       41   1                 5
       43 <210> SEQ ID NO: 3
       44 <211> LENGTH: 6
       45 <212> TYPE: PRT
       46 <213> ORGANISM: Artificial Sequence
       48 <220> FEATURE:
       49 <223> OTHER INFORMATION: Synthetic
       51 <400> SEQUENCE: 3
       52   Gly Thr Glu Pro Phe Thr
       53   1                 5
       55 <210> SEQ ID NO: 4
       56 <211> LENGTH: 5
       57 <212> TYPE: PRT
       58 <213> ORGANISM: Artificial Sequence
       60 <220> FEATURE:
       61 <223> OTHER INFORMATION: Synthetic
       63 <400> SEQUENCE: 4
       64   Ser Val Lys Ser Tyr
       65   1                 5
       67 <210> SEQ ID NO: 5
       68 <211> LENGTH: 6
       69 <212> TYPE: PRT
```

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/284,327**

DATE: 10/04/2001
TIME: 12:43:06

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\10042001\I284327.raw**

```
 70 <213> ORGANISM: Artificial Sequence
 72 <220> FEATURE:
 73 <223> OTHER INFORMATION: Synthetic
 75 <400> SEQUENCE: 5
 76  Lys Asn Phe Phe Asn Tyr
 77   1               5
 79 <210> SEQ ID NO: 6
 80 <211> LENGTH: 702
 81 <212> TYPE: DNA
 82 <213> ORGANISM: T. reesei
 84 <400> SEQUENCE: 6
 85  atgaagttcc ttcaagtcct ccctgccctc ataccggccg ccctggccca aaccagctgt        60
 86  gaccagtggg caaccttcac tggcaacggc tacacagtca gcaacaacct ttggggagca       120
 87  tcagccggct ctggatttgg ctgcgtgacg gcggtatcgc tcagcggcgg ggcctcctgg       180
 88  cacgcagact ggcagtggtc cggcggccag aacaacgtca agtcgtacca gaactctcag       240
 89  attgccattc cccagaagag gaccgtcaac agcatcagca gcatgcccac cactgccagc       300
 90  tggagctaca gcgggagcaa catccgcgct aatgttgcgt atgacttgtt caccgcagcc       360
 91  aacccgaatc atgtcacgta ctcgggagac tacgaactca tgatctggct tggcaaatac       420
 92  ggcgatattg ggccgattgg gtcctcacag gaacagtca acgtcggtgg ccagagctgg       480
 93  acgctctact atggctacaa cggagccatg caagtctatt cctttgtggc ccagaccaac       540
 94  actaccaact acagcggaga tgtcaagaac ttcttcaatt atctccgaga caataaagga       600
 95  tacaacgctg caggccaata tgttcttagc taccaatttg gtaccgagcc cttcacgggc       660
 96  agtggaactc tgaacgtcgc atcctggacc gcatctatca ac                         702
 98 <210> SEQ ID NO: 7
 99 <211> LENGTH: 232
100 <212> TYPE: PRT
101 <213> ORGANISM: T. reesei
103 <400> SEQUENCE: 7
104  Met Lys Phe Leu Gln Val Leu Pro Ala Leu Ile Pro Ala Ala Leu Ala
105   1               5                  10                  15
106  Gln Thr Ser Cys Asp Gln Trp Ala Thr Phe Thr Gly Asn Gly Tyr Thr
107              20                  25                  30
108  Val Ser Asn Asn Leu Trp Gly Ala Ser Ala Gly Ser Gly Phe Gly Cys
109              35                  40                  45
110  Val Thr Ala Val Ser Leu Ser Gly Gly Ala His Ala Asp Trp Gln Trp
111          50                  55                  60
112  Ser Gly Gly Gln Asn Asn Val Lys Ser Tyr Gln Asn Ser Gln Ile Ala
113  65                  70                  75                  80
114  Ile Pro Gln Lys Arg Thr Val Asn Ser Ile Ser Ser Met Pro Thr Thr
115                  85                  90                  95
116  Ala Ser Trp Ser Tyr Ser Gly Ser Asn Ile Arg Ala Asn Val Ala Tyr
117              100                 105                 110
118  Asp Leu Phe Thr Ala Ala Asn Pro Asn His Val Thr Tyr Ser Gly Asp
119              115                 120                 125
120  Tyr Glu Leu Met Ile Trp Leu Gly Lys Tyr Gly Asp Ile Gly Pro Ile
121          130                 135                 140
122  Gly Ser Ser Gln Gly Thr Val Asn Val Gly Gly Gln Ser Trp Thr Leu
123  145                 150                 155                 160
124  Tyr Tyr Gly Tyr Asn Gly Ala Met Gln Val Tyr Ser Phe Val Ala Gln
```

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PATENT APPLICATION: US/09/284,327   TIME: 12:43:06

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\10042001\I284327.raw

```
125                          165                 170                      175
126    Thr Asn Thr Thr Asn Tyr Ser Gly Asp Val Lys Asn Phe Phe Asn Tyr
127                180                     185                 190
128    Leu Arg Asp Asn Lys Gly Tyr Asn Ala Ala Gly Gln Tyr Val Leu Ser
129                195                     200                 205
130    Tyr Gln Phe Gly Thr Glu Pro Phe Thr Gly Ser Gly Thr Leu Asn Val
131                210                     215                 220
132    Ala Ser Trp Thr Ala Ser Ile Asn
133    225                      230
135 <210> SEQ ID NO: 8
136 <211> LENGTH: 234
137 <212> TYPE: PRT
138 <213> ORGANISM: T. reesei
140 <400> SEQUENCE: 8
141    Met Lys Phe Leu Gln Val Leu Pro Ala Leu Ile Pro Ala Ala Leu Ala
142    1                 5                     10              15
143    Gln Thr Ser Cys Asp Gln Trp Ala Thr Phe Thr Gly Asn Gly Tyr Thr
144                20                    25                  30
145    Val Ser Asn Asn Leu Trp Gly Ala Ser Ala Gly Ser Gly Phe Gly Cys
146                35                    40                  45
147    Val Thr Ala Val Ser Leu Ser Gly Gly Ala Ser Trp His Ala Asp Trp
148                50                    55                  60
149    Gln Trp Ser Gly Gly Gln Asn Asn Val Lys Ser Tyr Gln Asn Ser Gln
150    65                      70                    75                  80
151    Ile Ala Ile Pro Gln Lys Arg Thr Val Asn Ser Ile Ser Ser Met Pro
152                85                    90                  95
153    Thr Thr Ala Ser Trp Ser Tyr Ser Gly Ser Asn Ile Arg Ala Asn Val
154                100                   105                 110
155    Ala Tyr Asp Leu Phe Thr Ala Ala Asn Pro Asn His Val Thr Tyr Ser
156                115                   120                 125
157    Gly Asp Tyr Glu Leu Met Ile Trp Leu Gly Lys Tyr Gly Asp Ile Gly
158                130                   135                 140
159    Pro Ile Gly Ser Ser Gln Gly Thr Val Asn Val Gly Gly Gln Ser Trp
160    145                   150                   155                 160
161    Thr Leu Tyr Tyr Gly Tyr Asn Gly Ala Met Gln Val Tyr Ser Phe Val
162                165                   170                 175
163    Ala Gln Thr Asn Thr Thr Asn Tyr Ser Gly Asp Val Lys Asn Phe Phe
164                180                   185                 190
165    Asn Tyr Leu Arg Asp Asn Lys Gly Tyr Asn Ala Ala Gly Gln Tyr Val
166                195                   200                 205
167    Leu Ser Tyr Gln Phe Gly Thr Glu Pro Phe Thr Gly Ser Gly Thr Leu
168                210                   215                 220
169    Asn Val Ala Ser Trp Thr Ala Ser Ile Asn
170    225                      230
172 <210> SEQ ID NO: 9
173 <211> LENGTH: 234
174 <212> TYPE: PRT
175 <213> ORGANISM: H. schweinitzii
177 <400> SEQUENCE: 9
```

```
178   Met Lys Phe Leu Gln Val Leu Pro Ala Ile Leu Pro Ala Ala Leu Ala
179    1               5                  10                  15
180   Gln Thr Ser Cys Asp Gln Tyr Ala Thr Phe Ser Gly Asn Gly Tyr Ile
181               20                  25                  30
182   Val Ser Asn Asn Leu Trp Gly Ala Ser Ala Gly Ser Gly Phe Gly Cys
183           35                  40                  45
184   Val Thr Ser Val Ser Leu Asn Gly Ala Ala Ser Trp His Ala Asp Trp
185           50                  55                  60
186   Gln Trp Ser Gly Gly Gln Asn Asn Val Lys Ser Tyr Gln Asn Val Gln
187   65                  70                  75                  80
188   Ile Asn Ile Pro Gln Lys Arg Thr Val Asn Ser Ile Gly Ser Met Pro
189               85                  90                  95
190   Thr Thr Ala Ser Trp Ser Tyr Ser Gly Ser Asp Ile Arg Ala Asn Val
191               100                 105                 110
192   Ala Tyr Asp Leu Phe Thr Ala Ala Asn Pro Asn His Val Thr Tyr Ser
193           115                 120                 125
194   Gly Asp Tyr Glu Leu Met Ile Trp Leu Gly Lys Tyr Gly Asp Ile Gly
195           130                 135                 140
196   Pro Ile Gly Ser Ser Gln Gly Thr Val Asn Val Gly Gly Gln Thr Trp
197   145                 150                 155                 160
198   Thr Leu Tyr Tyr Gly Tyr Asn Gly Ala Met Gln Val Tyr Ser Phe Val
199               165                 170                 175
200   Ala Gln Ser Asn Thr Thr Ser Tyr Ser Gly Asp Val Lys Asn Phe Phe
201               180                 185                 190
202   Asn Tyr Leu Arg Asp Asn Lys Gly Tyr Asn Ala Gly Gly Gln Tyr Val
203           195                 200                 205
204   Leu Ser Tyr Gln Phe Gly Thr Glu Pro Phe Thr Gly Ser Gly Thr Leu
205           210                 215                 220
206   Asn Val Ala Ser Trp Thr Ala Ser Ile Asn
207   225                 230
209   <210> SEQ ID NO: 10
210   <211> LENGTH: 259
211   <212> TYPE: PRT
212   <213> ORGANISM: A. aculeatus
214   <400> SEQUENCE: 10
215   Met Lys Ala Phe His Leu Leu Ala Ala Leu Ala Gly Ala Ala Val Ala
216    1               5                  10                  15
217   Gln Gln Ala Gln Leu Cys Asp Gln Tyr Ala Thr Tyr Thr Gly Gly Val
218               20                  25                  30
219   Tyr Thr Ile Asn Asn Asn Leu Trp Gly Lys Asp Ala Gly Ser Gly Ser
220           35                  40                  45
221   Gln Cys Thr Thr Val Asn Ser Ala Ser Ser Ala Gly Thr Ser Trp Ser
222           50                  55                  60
223   Thr Lys Trp Asn Trp Ser Gly Gly Glu Asn Ser Val Lys Ser Tyr Ala
224   65                  70                  75                  80
225   Asn Ser Gly Leu Thr Phe Asn Lys Lys Leu Val Ser Gln Ile Ser Gln
226               85                  90                  95
227   Ile Pro Thr Thr Ala Arg Trp Ser Tyr Asp Asn Thr Gly Ile Arg Ala
228               100                 105                 110
```

RAW SEQUENCE LISTING   DATE: 10/04/2001
PATENT APPLICATION: US/09/284,327   TIME: 12:43:06

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\10042001\I284327.raw

```
229  Asp Val Ala Tyr Asp Leu Phe Thr Ala Ala Asp Ile Asn His Val Thr
230          115             120             125
231  Trp Ser Gly Asp Tyr Glu Leu Met Ile Trp Leu Ala Arg Tyr Gly Gly
232          130             135             140
233  Val Gln Pro Ile Gly Ser Gln Ile Ala Thr Ala Thr Val Asp Gly Gln
234  145             150             155             160
235  Thr Trp Glu Leu Trp Tyr Gly Ala Asn Gly Ser Gln Lys Thr Tyr Ser
236          165             170             175
237  Phe Val Ala Pro Thr Pro Ile Thr Ser Phe Gln Gly Asp Val Asn Asp
238          180             185             190
239  Phe Phe Lys Tyr Leu Thr Gln Asn His Gly Phe Pro Ala Ser Ser Gln
240          195             200             205
241  Tyr Leu Ile Thr Leu Gln Phe Gly Thr Glu Pro Phe Thr Gly Gly Pro
242          210             215             220
243  Ala Thr Leu Ser Val Ser Asn Trp Ser Ala Ser Val Gln Gln Ala Gly
244  225             230             235             240
245  Phe Glu Pro Trp Gln Asn Gly Ala Gly Leu Ala Val Asn Ser Phe Ser
246          245             250             255
247  Ser Thr Val
250  <210> SEQ ID NO: 11
251  <211> LENGTH: 239
252  <212> TYPE: PRT
253  <213> ORGANISM: A. kawachii
255  <400> SEQUENCE: 11
256  Met Lys Leu Ser Met Thr Leu Ser Leu Phe Ala Ala Thr Ala Met Gly
257  1               5               10              15
258  Gln Thr Met Cys Ser Gln Tyr Asp Ser Ala Ser Ser Pro Pro Tyr Ser
259          20              25              30
260  Val Asn Gln Asn Leu Trp Gly Glu Tyr Gln Gly Thr Gly Ser Gln Cys
261          35              40              45
262  Val Tyr Val Asp Lys Leu Ser Ser Ser Gly Ala Ser Trp His Thr Lys
263          50              55              60
264  Trp Thr Trp Ser Gly Gly Glu Gly Thr Val Lys Ser Tyr Ser Asn Ser
265  65              70              75              80
266  Gly Leu Thr Phe Asp Lys Lys Leu Val Ser Asp Val Ser Ser Ile Pro
267          85              90              95
268  Thr Ser Val Thr Trp Ser Gln Asp Asp Thr Asn Val Gln Ala Asp Val
269          100             105             110
270  Ser Tyr Asp Leu Phe Thr Ala Ala Asn Ala Asp His Ala Thr Ser Ser
271          115             120             125
272  Gly Asp Tyr Glu Leu Met Ile Trp Leu Ala Arg Tyr Gly Ser Val Gln
273          130             135             140
274  Pro Ile Gly Lys Gln Ile Ala Thr Ala Thr Val Gly Gly Lys Ser Trp
275  145             150             155             160
276  Glu Val Trp Tyr Gly Thr Ser Thr Gln Ala Gly Ala Glu Gln Lys Thr
277          165             170             175
278  Tyr Ser Phe Val Ala Gly Ser Pro Ile Asn Ser Trp Ser Gly Asp Ile
279          180             185             190
280  Lys Asp Phe Phe Asn Tyr Leu Thr Gln Asn Gln Gly Phe Pro Ala Ser
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/284,327**

DATE: 10/04/2001
TIME: 12:43:07

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\10042001\I284327.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date